the efficacy of a particular treatment for subjects who have the protein in the database is known.

70 ~~68~~. (New) The method of claim ~~67~~ 69, wherein the protein is an human immunodeficiency virus (HIV) protein.

71 ~~70~~. (New) The method of claim ~~69~~ 70, wherein the HIV protein is a protease or reverse transcriptase.

72 ~~71~~. (New) The method of claim ~~67~~ 68, wherein the primary sequence of the target protein is deduced from the sequence of a gene obtained from a subject sample.

73 ~~72~~. (New) The method of claim ~~67~~ 69, wherein the subject is a human.

74 ~~73~~. (New) The method of claim ~~67~~ 68, wherein the protein is encoded by gene that has a plurality of polymorphisms.

75 ~~74~~. (New) A method for predicting resistance or susceptibility to a particular drug therapy, comprising:

generating a 3-D structural model of a target protein from a subject;

performing protein-drug binding analyses *in silico*; and

predicting drug sensitivity or resistance based on the protein-drug binding analyses.

76 ~~75~~. (New) The method of claim ~~74~~ 75, wherein the protein is an HIV protein.

77 ~~76~~. (New) The method of claim ~~76~~ 75, wherein the HIV protein is a protease or reverse transcriptase.

78 ~~77~~. (New) The method of claim ~~74~~ 75, wherein the primary sequence of the target protein is deduced from the sequence of a gene obtained from a subject sample.

79 ~~78~~. (New) The method of claim ~~74~~ 75, wherein the subject is a human.

80 79. (New) A method for predicting clinical responses in subjects based on genetic polymorphisms, comprising:

comparing a 3-D model of the structure of a protein from biological sample from a subject to 3-D structures contained in a database of claim 38;

identifying structures in the database that are similar to the model of the protein from the subject; and

predicting a clinical outcome for the subject based on the clinical data associated with the identified structures.

81 80. (New) The method of claim 74 75, wherein the subject is a human.

82 81. (New) A computer-based method of selecting drug therapies for subjects based on a genetic polymorphism, comprising:

determining the amino acid sequence of a protein from a biological sample from a subject;

identifying a structural variant model with the same amino acid sequence or similar 3-dimensional (database) structure in a database of three-dimensional structural variants;

selecting a drug therapy for the subject based on the drug or drugs that have the most favorable binding interactions with the structural variant model that corresponds to the protein in the subject sample.

83 82. (New) The method of claim 80 81, wherein the protein is encoded by gene that has a plurality of polymorphisms.

84 83. (New) A computer-based method of selecting drug therapies for subjects based on a genetic polymorphism, comprising:

determining the amino acid sequence of a protein from a biological sample from a subject;

identifying a structural variant model with the same amino acid sequence or the same or similar 3-dimensional (3-D) structure in a database of claim 38; 39

C1

selecting a drug therapy for the subject based on the drug or drugs that have the most favorable binding interactions with the structural variant model that corresponds to the protein in the subject sample.

85 ~~84~~. (New) The method of claim ~~83~~ 84, wherein the subject is a human.

86 ~~85~~. (New) The method of claim ~~83~~ 84, wherein the protein is encoded by gene that has a plurality of polymorphisms.

87 ~~86~~. (New) The method of claim 1, wherein the selected subpopulation is a human patient subpopulation.

sub F29 88 ~~87~~. (New) The method of claim ~~19~~ 20, wherein the selected subpopulation is a human patient subpopulation.

89 ~~88~~. (New) The method of claim ~~20~~ 21, wherein a subject is a human.

90 ~~89~~. (New) The method of claim ~~21~~ 22, wherein a subject is a human.

91 ~~90~~. (New) The method of claim ~~25~~ 26, wherein a subject is a human.

92 ~~91~~. (New) The method of claim ~~28~~ 29, wherein a subject is a human.

C1 93 ~~92~~. (New) The method of claim ~~30~~ 31, wherein a subject is a human.

94 ~~93~~. (New) The method of claim ~~80~~ 81, wherein the subject is a human.

Please replace claims 11, 12, 19-21, 25, 27, 28 and 30 with amended claims 11, 12, 19-21, 25, 27, 28 and 30 as follows:

C2 12 ~~11~~. (Amended) The method of claim 1, wherein the selected model structures represent the structural variants resulting from genetic polymorphisms found in a selected subpopulation.

13 ~~12~~. (Amended) The method of claim 1, wherein the structural variant models are stored in a relational database, comprising:

3-D molecular coordinates for the structural variants;

a molecular graphics interface for 3-D molecular structure visualization; computer functionality for protein sequence and structural analyses; and

database searching tools.

C3 20 ~~19~~. (Amended) The method of claim 18 ~~17~~, wherein the selected model structures represent the structural variants resulting from genetic polymorphisms found in a subpopulation.

21 ~~20~~. (Twice Amended) The method of claim 13 ~~12~~, wherein the selected model structures represent structural variants derived from subjects who receive a specific treatment regimen.

C4 22 ~~21~~. (Twice Amended) The method of claim 13 ~~12~~, wherein the selected model structures represent structural variants derived from subjects who exhibit a particular clinical response to a given drug.

25 ~~24~~. (Amended) A computer-based method of selecting drug therapies for subjects based on genetic polymorphisms, comprising:

obtaining amino acid sequences of a target protein that is the product of a gene exhibiting genetic polymorphisms, wherein the sequences represent different genetic polymorphisms;

C5 generating 3-D protein structural variant models from the sequences;

computationally docking drug molecules with the target protein models;

energetically refining the docked complexes;

determining the binding interactions between the drug or potential new drug candidate molecules and the models; and

selecting drug therapies based on the drug or drugs that have the most favorable binding interactions with the structural variant models.

C6 28 ~~27~~. (Amended) The method of claim 1, further comprising:

after generating the 3-D structural variant models, exporting some or all of them models into a program that computationally docks the models with test compounds to assess intermolecular interactions.

C7 29 ~~28~~. (Amended) A computer-based method for predicting clinical responses in subjects based on genetic polymorphisms, comprising:

obtaining one or more amino acid sequences for a target protein that is the product of a gene exhibiting genetic polymorphisms;

generating 3-D protein structural variant models from the sequences;

building a relational database of protein structural variants derived based on genetic polymorphisms and observed clinical data associated with particular polymorphisms exhibited in the subjects, wherein the database comprises:

3-D molecular coordinates for the structural variant models;

a molecular graphics interface for 3-D molecular structure visualization;

computer functionality for protein sequence and structural analysis; database searching tools; and

observed clinical data associated with the genetic polymorphisms, subject medical history and subject history associated with the genetic polymorphisms;

obtaining a target protein structural variant based on the same gene associated with a polymorphism in a subject;

generating a 3-D protein model based on the subject's gene sequence;

screening/comparing the 3-D model derived from the subject to the structures contained in the database by:

identifying structures in the database that are similar to the model derived from the subject; and

predicting a clinical outcome for the subject based on the clinical data associated with the identified structures.

31 ~~30~~. (Amended) A computer-based method for identifying compensatory mutations in a target protein, comprising:

obtaining the amino acid sequence of a target protein containing multiple amino acid mutations that is expressed in a patient, wherein the structure of a